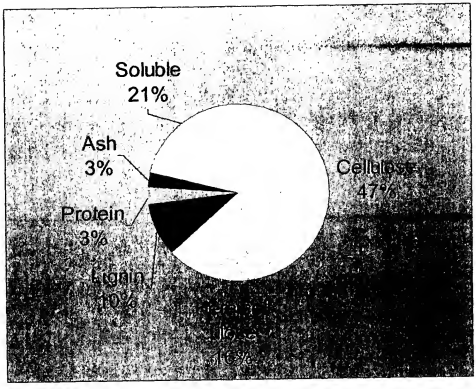

Figure 1.

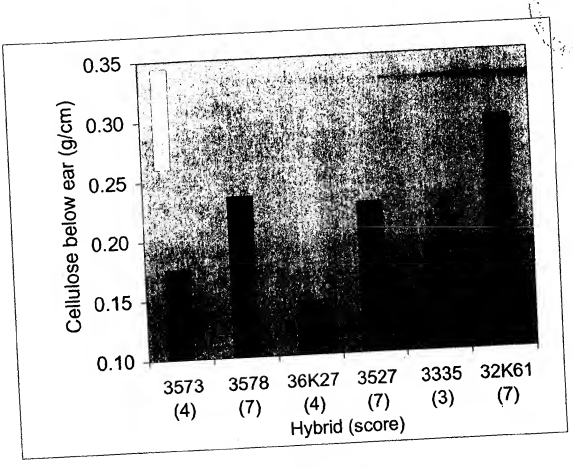
0.35
0.30
0.25
0.20
0.15
0.10
Cellulose below ear (g/cm)
3573 (4)
3578 (7)
36K27 (4)
3527 (7)
3335 (3)
32K61 (7)
Hybrid (score)

Figure 2

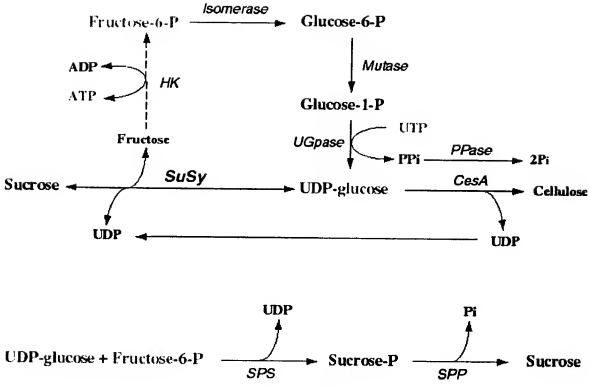
Fructose-6-P
Isomerase
Glucose-6-P
ADP
ATP
HK
Mutase
Glucose-1-P
Fructose
UTP
UGpase
PPi
PPase
2Pi
Sucrose
SuSy
UDP-glucose
CesA
Cellulose
UDP
UDP
UDP-glucose + Fructose-6-P
UDP
SPS
Sucrose-P
Pi
SPP
Sucrose

Figure 3.

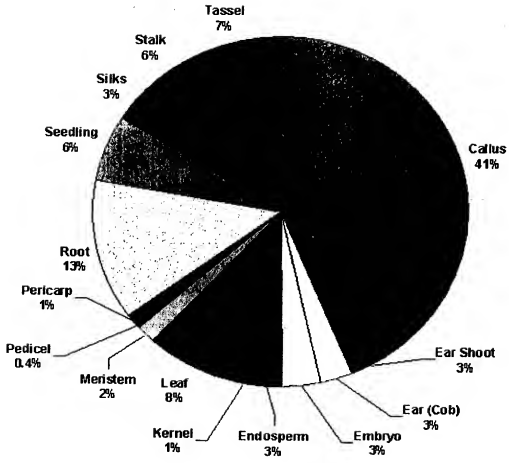
Tassel
7%
Stalk
6%
Silks
3%
Seedling
6%
Callus
41%
Root
13%
Pericarp
1%
Pedicel
0.4%
Meristem
2%
Leaf
8%
Kernel
1%
Endosperm
3%
Embryo
3%
Ear (Cob)
3%
Ear Shoot
3%

Figure 4.

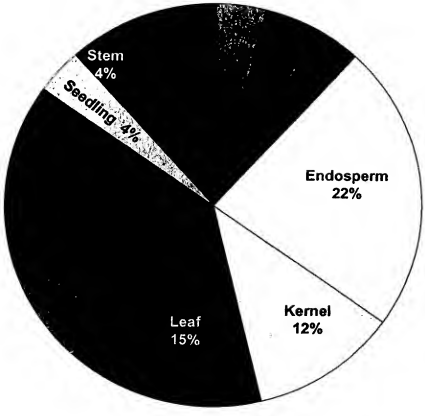

Figure 5

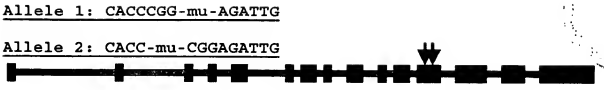

Figure 6.

Genotype	structural dry matter (% of total dry matter)	cellulose (% of total dry matter)	cellul s (% f structural dry matter)
Sus-1 (WT)	63.2	25.2 +/-0.38	39.9
sus-1 (mutant)	47.3	17.7 +/-0.34	37.4

Figure 7.

```
                     1                                                50
Sh1         (1)  -----MAAKLTRLHSLRERLGATFSSHPNELIALFSRYVHQGKGMLQRHQ
Sus1        (1)  MGEGAGDRVLSRLHSVRERIGDSLSAHPNELVAVFTRLKNLGKGMLQPHQ
Sus3        (1)  -----------STHASGDRVEDTLHAHRNELVALLSKYVNKGKGILQPHH
Consensus   (1)           LSRLHSLRERIGDTLSAHPNELVALFSRYVN GKGMLQPHQ
                 51                                              100
Sh1        (46)  ILAEFD-ALFDSDKE--KYAPFEDTLRAAQEAIVLPPWVALAIRPRPGVW
Sus1       (51)  IIAEYNNAIPEAEREKLKDGAFEDVLRAAQEAIVIPPWVALAIRPRPGVW
Sus3       (40)  ILDALDEVQGSGGRA-LAEGPFLDVLRSAQEAIVLPPFVALAVRPRPGVW
Consensus  (51)  ILAEFD AI DADRE LKDGPFEDVLRAAQEAIVLPPWVALAIRPRPGVW
                 101                                             150
Sh1        (93)  DYIRVNVSELAVEELSVSEYLAFKEQLVDGQSNSNF[illegible]NASFP
Sus1      (101)  EYVRVNVSELAVEELRVPEYLQFKEQLVEEGPNNNF[illegible]ASFP
Sus3       (89)  EYVRVNVHELSVEQLTVSEYLRFKEELVDGQHNDPY[illegible]V[illegible]
Consensus (101)  EYVRVNVSELAVEELSVSEYL FKEQLVDGQ N NFVLELDFEPFNASFP
                 151                                             200
Sh1       (143)  [illegible]S[illegible]K[illegible]KLFQDKESLY[illegible]N[illegible]A[illegible]NY[illegible]TT[illegible]
Sus1      (151)  [illegible]S[illegible]K[illegible]KLFHDKESMY[illegible]N[illegible]RA[illegible]NY[illegible]MT[illegible]
Sus3      (139)  [illegible]NR[illegible]S[illegible]I[illegible]RN[illegible]CLE[illegible]D[illegible]R[illegible]R[illegible]HV[illegible]
Consensus (151)  RPSLSKSIGNGVQFLNRHLSSKLF DKESLYPLLNFLRAHNYKG TMMLN
                 201                                             250
Sh1       (193)  [illegible]Q[illegible]R[illegible]S[illegible]R[illegible]L[illegible]PQ[illegible]E[illegible]NHR[illegible]L[illegible]T[illegible]K
Sus1      (201)  [illegible]R[illegible]S[illegible]G[illegible]R[illegible]H[illegible]S[illegible]LQA[illegible]E[illegible]HHR[illegible]L[illegible]C[illegible]K
Sus3      (189)  [illegible]Q[illegible]GR[illegible]SV[illegible]T[illegible]H[illegible]SKLPA[illegible]Q[illegible]A[illegible]W[illegible]T[illegible]G
Consensus (201)  DRIQSL ALQSALRKAEEHLSSLPADTPYSEF HRFQELGLEKGWGDTAK
                 251                                             300
Sh1       (243)  RVL[illegible]T[illegible]LLE[illegible]AN[illegible]T[illegible]IL[illegible]A[illegible]
Sus1      (251)  RAQETI[illegible]LLE[illegible]ST[illegible]T[illegible]IL[illegible]A[illegible]A[illegible]
Sus3      (239)  HVLEMI[illegible]ST[illegible]R[illegible]A[illegible]
Consensus (251)  RVLETIHLLLDLLEAPDPSTLEKFLGTIPMIFNVVILSPHGYFAQANVLG
                 301                                             350
Sh1       (293)  Y[illegible]LENEMLLRIKQQ[illegible]IT[illegible]L[illegible]A[illegible]
Sus1      (301)  Y[illegible]MENEMLLRIKQC[illegible]IT[illegible]L[illegible]T[illegible]
Sus3      (289)  L[illegible]KQ[illegible]K[illegible]
Consensus (301)  YPDTGGQVVYILDQVRALENEMLLRIKQQGLDITPKILIVTRLLPDA GT
                 351                                             400
Sh1       (343)  TCGQRLEKVIGTEHTDIIRVPFRNENGILRKWISRFD[illegible]YTE[illegible]VS
Sus1      (351)  TCGQRLEKVLGTEHCHILRVPFRTENGIVRK[illegible]YTDDVA
Sus3      (339)  SCNQRLERISGTQHTYILRVPFRNENGILKKWISRFD[illegible]AE[illegible]AA
Consensus (351)  TCGQRLEKVIGTEHTHILRVPFRNENGILRKWISRFDVWPYLETYTEDVA
                 401                                             450
Sh1       (393)  SEIMKEMQAKPDLIIGNYSDGNLVATLLAHKLGVTQCTIAHALEKTKYPN
Sus1      (401)  HEIAGELQANPDLIIGNYSDGNLVACLLAHKMGVTHCTIAHALEKTKYPN
Sus3      (389)  GEIAAELQGTPDFIIGNYSDGNLVASLLSYKMGITQCNIAHALEKTKYPD
Consensus (401)   EIAAELQA PDLIIGNYSDGNLVASLLAHKMGVTQCTIAHALEKTKYPN
                 451                                             500
Sh1       (443)  SDIYLDKFDSQYHFSCQFTADLIAMNHTDFIITSTFQEIAGSKDTVGQYE
Sus1      (451)  SDLYWKKFEDHYHFSCQFTTDLIAMNHADFIITSTFQEIAGNKDTVGQYE
Sus3      (439)  SDIFWKNFDEKYHFSCQFTADIIAMNNADFIITSTYQEIAGSKNTVGQYE
Consensus (451)  SDIYWKKFDD YHFSCQFTADLIAMNHADFIITSTFQEIAGSKDTVGQYE
                 501                                             550
Sh1       (493)  SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSVYYPYTETDKRLTAFH
Sus1      (501)  SHMAFTMPGLYRVVHGIDVFDPKFNIVSPGADLSIYFPYTESHKRLTSLH
Sus3      (489)  SHTAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPHTEKAKRLTSLH
Consensus (501)  SHIAFTLPGLYRVVHGIDVFDPKFNIVSPGADMSIYFPYTES KRLTSLH
```

Figure 8a


551 600
Sh1 (543) PETEELIYSDVENSEHKFVLKDKKKPIIFSMARLDRVKNMTGLVEMYGKN
Sus1 (551) PETEELLYSQTENTEHKFVLNDRNKPIIFSMARLDRVKNLTGLVELYGRN
Consensus (551) PEIEELIYS ENSEHKFVL DR KPIIFSMARLDRVKNITGLVELYGKN
601 650
Sh1 (593) ARLRELANLVIVAGDHGK-ESKDREEQAEFKKMYSLIDEYKLKGHIRWIS
Sus1 (601) KRLQELVNLVVVCGDHGN-PSKDKEEQAEFKKMFDLIEQYNLNGHIRWIS
Sus3 (589) AKLRELVNLVVVAGYNDVNKSKDREEIAEIEKMHELIKTHNLFGQFRWIS
Consensus (601) ARLRELVNLVVVAGDHG SKDREEQAEFKKMHDLID YNL GHIRWIS
651 700
Consensus (651) AQMNRVRNGELYRYICDTKGAFVQPAFYEAFGLTVVEAMTCGLPTFAT H
701 750
Consensus (701) GGPAEIIVHGVSGFHIDPYH DKAA LLVDFFDKCKADPSHW ISQGGL
751 800
Consensus (751) QRIYEKYTWKLYSERLMTLTGVYGFWKYVSNLERRETRRYLEMFYALKYR
801 817
Consensus (801) SLASTVPLAID P

Figure 8b

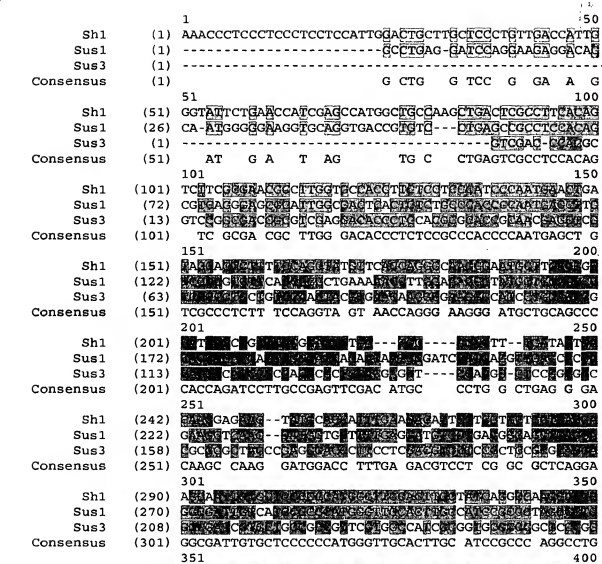

Figure 9a

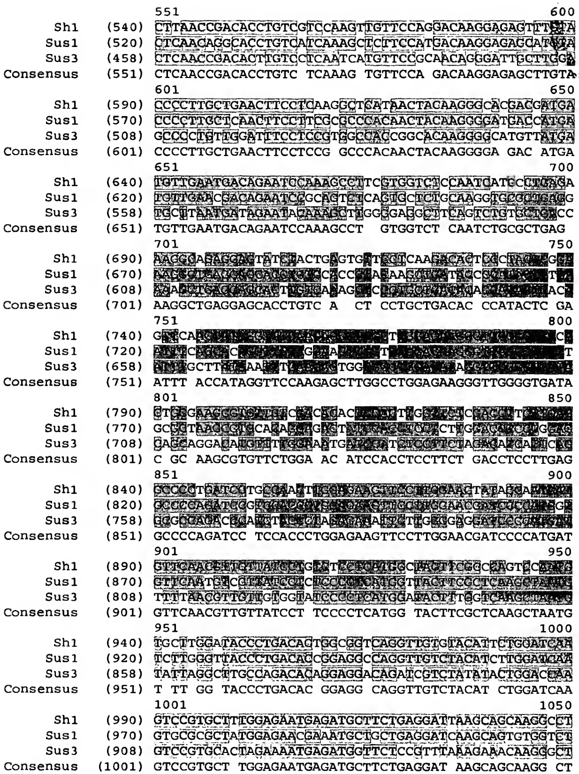
551 600
Sh1 (540) CTTAACCGACACCTGTCGTCCAAGTTGTTCCAGGACAAGGAGAGTTT
Sus1 (520) CTCAACAGGCACCTGTCATCAAAGCTCTTCCATGACAAGGAGAGCAT
Sus3 (458) CTCAACCGACACTTGTCCTCAATCATGTTCCGCAACAGGGATTGCTTGC
Consensus (551) CTCAACCGACACCTGTC TCAAAG TGTTCCA GACAAGGAGAGCTTGTA
601 650
Sh1 (590) CCCCTTGCTGAACTTCCTCAAGGCTCATAACTACAAGGGCACGACGATGA
Sus1 (570) CCCCTTGCTCAACTTCCTTCGCGCCCACAACTACAAGGGGATGACCATGA
Sus3 (508) GCCCCTGTTGGATTTCCTCCGTGGCCAGCGGCACAAGGGGCATGTTATGA
Consensus (601) CCCCTTGCTGAACTTCCTCCG GCCCACAACTACAAGGGGA GAC ATGA
651 700
Sh1 (640)
Sus1 (620)
Sus3 (558)
Consensus (651) TGTTGAATGACAGAATCCAAAGCCT GTGGTCT CAATCTGCGCTGAG
701 750
Sh1 (690)
Sus1 (670)
Sus3 (608)
Consensus (701) AAGGCTGAGGAGCACCTGTC A CT CCTGCTGACAC CCATACTC GA
751 800
Sh1 (740)
Sus1 (720)
Sus3 (658)
Consensus (751) ATTT ACCATAGGTTCCAAGAGCTTGGCCTGGAGAAGGGTTGGGGTGATA
801 850
Sh1 (790)
Sus1 (770)
Sus3 (708)
Consensus (801) C GC AAGCGTGTTCTGGA AC ATCCACCTCCTTCT GACCTCCTTGAG
851 900
Sh1 (840)
Sus1 (820)
Sus3 (758)
Consensus (851) GCCCCAGATCC TCCACCCTGGAGAAGTTCCTTGGAACGATCCCCATGAT
901 950
Sh1 (890)
Sus1 (870)
Sus3 (808)
Consensus (901) GTTCAACGTTGTTATCCT TCCCCTCATGG TACTTCGCTCAAGCTAATG
951 1000
Sh1 (940) TGCTTGGATACCCTGACAGTGGCGGTCAGGTTGTGTACATTCTGGATCAA
Sus1 (920) TCTTGGGTTACCCTGACACCGGAGGCCAGGTTGTCTACATCTTGGATCAA
Sus3 (858) TATTAGGCTTGCCAGACACAGGAGGACAGATCGTCTATATACTGGACCAA
Consensus (951) T TT GG TACCCTGACAC GGAGG CAGGTTGTCTACAT CTGGATCAA
1001 1050
Sh1 (990) GTCCGTGCTTTGGAGAATGAGATGCTTCTGAGGATTAAGCAGCAAGGCCT
Sus1 (970) GTGCGCGCTATGGAGAACGAAATGCTGCTGAGGATCAAGCAGTGTGGTCT
Sus3 (908) GTCCGTGCACTAGAAAATGAGATGGTTCTCCGTTTAAAGAAACAAGGCCT
Consensus (1001) GTCCGTGCT TGGAGAATGAGATGCTTCTGAGGAT AAGCAGCAAGG CT

Figure 9b

```
                     1051                                              1100
      Sh1   (1040)  TGATATCACTCCGAAGATCCTCATTGTTACCAGGCTGTTGCCTGATGCTG
     Sus1   (1020)  TGACATCACGCCGAAGATCCTTATTGTCACCAGGTTGCTCCCTGATGCAA
     Sus3    (958)  TGATGTTTCCCCAAAGATTCTCATTGTTACTCGGCTGA[illegible]
Consensus   (1051)  TGATATCAC CCGAAGATCCTCATTGTTACCAGGCTG T CCTGATGCAA

                     1101                                              1150
      Sh1   (1090)  CTGGACTACGTGCGGTCAGCGGCTGGAGAAGGTCATTGGTAGTGAGCAC
     Sus1   (1070)  CTGGCACCACCTGTGGCCAGCGCCTTGAGAAGGTCCTTGGCACCGAGCAC
     Sus3   (1008)  AAGGAACATCATGCAATCAGCGGCTTGAGAGAATTAGTGGAAGACAGCAT
Consensus   (1101)  CTGG AC AC TGCGGTCAGCGGCTTGAGAAGGTCATTGG AC GAGCAC
                     1151                                              1200
      Sh1   (1140)  ACAGACATCATTCGCGTTCCCTTCAGAAATGAGAATGGCATCC[illegible]
     Sus1   (1120)  TGCCATATCCTTCGCGTGCCATTCATAACAGAAAACGGATTCG[illegible]
     Sus3   (1058)  ACTTACATATTACGAGTT[illegible]G[illegible]A[illegible]AAG[illegible]
Consensus   (1151)  AC  ACATC TTCGCGTTCCCTTCAGAAATGAAAATGG ATCCTTCGCAA
                     1201                                              1250
      Sh1   (1190)  GTGGATCTGTCGTTTT[illegible]
     Sus1   (1170)  GTGGATCTCGGCATTTGA[illegible]G[illegible]T[illegible]T
     Sus3   (1108)  ATGGATATCAAGAT[illegible]G[illegible]T[illegible]A[illegible]TTG[illegible]
Consensus   (1201)  GTGGATCTC CGATTTGATGTCTGGCCATACCTGGAGACATACACTGAGG
                     1251                                              1300
      Sh1   (1240)  ATGTTTTCCAGTGAAATAATGAA[illegible]A[illegible]G[illegible]G[illegible]T[illegible]
     Sus1   (1220)  ACGTGGCGCATGAGATTGC[illegible]G[illegible]GC[illegible]T[illegible]G[illegible]
     Sus3   (1158)  ATGCTGCTGGTGAAATTGCTGCT[illegible]T[illegible]A[illegible]GT[illegible]C[illegible]A[illegible]T[illegible]C[illegible]A
Consensus   (1251)  ATGTTGC  GTGAAATTGCTG AGAA T CAGGCCAATCCTGACCT ATC
                     1301                                              1350
      Sh1   (1290)  ATTGGCAACTACAGCCGATGGC[illegible]A[illegible]C[illegible]CA[illegible]C[illegible]G[illegible]
     Sus1   (1270)  ATCGGAAACTACAGTGACCGGAAAC[illegible]T[illegible]G[illegible]C[illegible]
     Sus3   (1208)  ATTGGAAACTACAGTGATGGAA[illegible]T[illegible]G[illegible]AT[illegible]AT[illegible]TT[illegible]
Consensus   (1301)  ATTGGAAACTACAGTGATGGAAACCTTGT GCGTCTTTGCTCGC CACAA
                     1351                                              1400
      Sh1   (1340)  GTTGGGAGTCACTCACT[illegible]C[illegible]CT[illegible]C[illegible]A[illegible]
     Sus1   (1320)  GATGGGTGTTACTCAC[illegible]C[illegible]GCTT[illegible]
     Sus3   (1258)  GATGGAATTACCCAGTGCAA[illegible]T[illegible]A[illegible]G[illegible]
Consensus   (1351)  GATGGGAGTTACTCAGTGTACCATTGCTCATGC CTGGAGAAAACTAAGT
                     1401                                              1450
      Sh1   (1390)  ACCCCAACTCGGACATCTACTTGGACAAATTCGACAGCCAGTACCACTTC
     Sus1   (1370)  ACCCTAACTCCGACCTCTACTGGAAGAAGTTTGAGGATCACTACCACTTC
     Sus3   (1308)  ATCCAGATTCAGACATATTTTGGAAGAATTTCGATGAGAAGTACCATTTC
Consensus   (1401)  ACCC AACTC GACATCTACTGGAAGAA TTCGA GA CAGTACCACTTC
                     1451                                              1500
      Sh1   (1440)  TCTTGCCAGTTCACAGCTGACCTTATTGCCATGAACCACACCGATTTCAT
     Sus1   (1420)  TCGTGCCAGTTCACCACTGACTTGATTGCAATGAACCATGCCGACTTCAT
     Sus3   (1358)  TCCTGCCAGTTCACTGCTGATATAATTGCTATGAACAATGCTGATTTTAT
Consensus   (1451)  TC TGCCAGTTCAC GCTGAC T ATTGC ATGAACCATGCCGATTTCAT
                     1501                                              1550
      Sh1   (1490)  CATCACCAGCACATTCCAAGAAATCGCGGAAGCAAGGACACCGTGGGC
     Sus1   (1470)  CATCACCAGTACCTTCCAAGAGATCGCCGGAAACAAGGACACCGTCGGCC
     Sus3   (1408)  CATCACCAGCACATACCAAGAAATTGCTGGAAGCAAAAATACTGTTGGAC
Consensus   (1501)  CATCACCAGCACATTCCAAGAAATCGC GGAAGCAAGGACACCGT GG C
```

Figure 9c

```
                 1551                                              1600
Sh1       (1540) AGTACGAGTCCCATATCGCGTTCACTCTTCCTGGGCTCTACCGTGTC[illegible]
Sus1      (1520) AGTACGAGTCACACATGGCGTTCACAATGCCTGGCCTGTACCGC[illegible]
Sus3      (1458) AGTATGAGAGTCATACTGCCTTTACTCTGCCTGGTCTGTACCGAGTTGTG
Consensus (1551) AGTACGAGTC CATAT GCGTTCACTCTGCCTGG CTGTACCG GTTGTC
                 1601                                              1650
Sh1       (1590) CATGGCATCGATGTTTTCGATCCCAAGTTCAAGATT[illegible]
Sus1      (1570) CACGGCATTGATGTGTTCGACCCCAAGTTGAACATCGTG[illegible]CGC
Sus3      (1508) CATGGGATCGATGTCTTCGATCCAAAGTTCAATATA[illegible]
Consensus (1601) CATGGCATCGATGT TTCGATCCCAAGTTCAACAT GTCTCTCCTGGAGC
                 1651                                              1700
Sh1       (1640) AGACATGAGTGTTTACTACCCTTATACGGAAAACGA[illegible]TG
Sus1      (1620) GGACCTGTCCATCTACTTCCCGTACACCGAGTTGCA[illegible]G[illegible]
Sus3      (1558) TGACATGTCCATATACTTTTCCACATACCGAGAAGGCAC[illegible]C[illegible]
Consensus (1651)  GACATGTCCAT TACTTCCC TATACCGAGACGGACAAGAGACTCACCT
                 1701                                              1750
Sh1       (1690) CCT[illegible]C[illegible]C[illegible]G[illegible]C[illegible]T[illegible]TC
Sus1      (1670) [illegible]CCGGGAG[illegible]C[illegible]G[illegible]AAC[illegible]AG
Sus3      (1608) GT[illegible]GGTTC[illegible]AA[illegible]TT[illegible]G[illegible]T[illegible]TGA[illegible]CG[illegible]AGC[illegible]A[illegible]GAT
Consensus (1701) CCCTTCATCCTGAAATCGAGGAGCTCAT TACAGCCA G CGAGAAC C
                 1751                                              1800
Sh1       (1740) [illegible]G[illegible]G[illegible]A[illegible]G[illegible]G[illegible]G
Sus1      (1720) [illegible]C[illegible]C[illegible]A[illegible]
Sus3      (1658) [illegible]TTGGGCA[illegible]G[illegible]T[illegible]C[illegible]TCA[illegible]C[illegible]C[illegible]
Consensus (1751) GAGCACAAGTTCGTTCTGAA GACAGGAA AAGCC ATCATCTTCTCCAT
                 1801                                              1850
Sh1       (1790) GGCGCGTCTCGACCGC[illegible]C[illegible]A[illegible]
Sus1      (1770) GGCTCGTCTCGACCGT[illegible]T[illegible]T[illegible]G[illegible]C[illegible]
Sus3      (1708) GGCAAGACTCGACAGG[illegible]A[illegible]AGCT[illegible]TT
Consensus (1801) GGC CGTCTCGACCG GTGAAGAACATGACAGGGCTGGTCGAG TGTACG
                 1851                                              1900
Sh1       (1840) GCAAGAACGCGCGCCTGAGG[illegible]C[illegible]A[illegible]T
Sus1      (1820) GCCGGAAGAAGCGGCTGCA[illegible]CTG[illegible]C
Sus3      (1758) CTAAGTGCGGCTAAGCTGA[illegible]A[illegible]T[illegible]C[illegible]G
Consensus (1851) GCAAGAACGCGCGGCTGAGGGAGCTGGTGAACCTCGTGGTCGTTGCCGG
                 1901                                              1950
Sh1       (1890) GACCACGG---CAAGGA[illegible]
Sus1      (1870) GACCATGG---CAACCCTTCCAAGGA[illegible]A[illegible]C[illegible]
Sus3      (1808) TACAATGATGTCAACAAGTCCAAGGACAGCGGA[illegible]ATC[illegible]A[illegible]AG[illegible]
Consensus (1901) GACCATGG   CAAC AGTCCAAGGACAGGGAGGAGCAGGCGGAGTTCAA
                 1951                                              2000
Sh1       (1937) GAAGATGTACAGCCTCATCGACGAGTACAAGC[illegible]GC[illegible]C[illegible]TA[illegible]GC
Sus1      (1917) GAAGATGTTTGACCTCATCGAGCAGTACAACC[illegible]C[illegible]
Sus3      (1858) GAAGATGCATGAACTCATCAAGACCCACAACTTGTT[illegible]GT[illegible]CT
Consensus (1951) GAAGATGTATGACCTCATCGAG AGTACAACTTGAACGGGCA ATCCGCT
                 2001                                              2050
Sh1       (1987) GGATCTCGGCGCAGATGAACCGTGTCCGCAACGGCGAGCTGTACCGCTAC
Sus1      (1967) GGATCTCCGCCCAGATGAACCGCGTCCGCAACGGCGAGATGTACCGCTAC
Sus3      (1908) GGATCTCTGCCCAGACAAACAGGGCCCGTAACGGCGAGCTCTATCGGTAC
Consensus (2001) GGATCTC GCCCAGATGAACCG GTCCGCAACGGCGAGCTGTACCGCTAC
                 2051                                              2100
Sh1       (2037) ATTTGCGATACCAAGGGCGCATTCGTGCAGCCTGCGTTCTACGAAGCGTT
Sus1      (2017) ATCTGCGACACCAAGGGCGCCTTCGTGCAGCCTGCTTTCTACGAGGCTTT
Sus3      (1958) ATCGCTGATACCCATGGTGCTTTCGTACAGCCGGCCTTGTATGAAGCGTT
Consensus (2051) ATCTGCGATACCAAGGGCGC TTCGTGCAGCCTGC TTCTACGAAGCGTT
```

Figure 9d

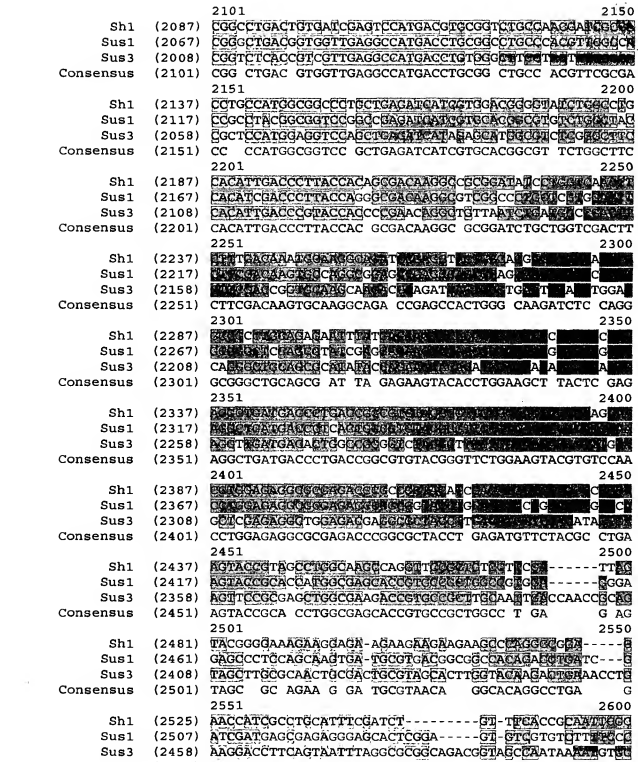
2101 2150
Sh1 (2087)
Sus1 (2067)
Sus3 (2008)
Consensus (2101) CGG CTGAC GTGGTTGAGGCCATGACCTGCGG CTGCC ACGTTCGCGA
2151 2200
Sh1 (2137)
Sus1 (2117)
Sus3 (2058)
Consensus (2151) CC CCATGGCGGTCC GCTGAGATCATCGTGCACGGCGT TCTGGCTTC
2201 2250
Sh1 (2187)
Sus1 (2167)
Sus3 (2108)
Consensus (2201) CACATTGACCCTTACCAC GCGACAAGGC GCGGATCTGCTGGTCGACTT
2251 2300
Sh1 (2237)
Sus1 (2217)
Sus3 (2158)
Consensus (2251) CTTCGACAAGTGCAAGGCAGA CCGAGCCACTGGG CAAGATCTC CAGG
2301 2350
Sh1 (2287)
Sus1 (2267)
Sus3 (2208)
Consensus (2301) GCGGGCTGCAGCG AT TA GAGAAGTACACCTGGAAGCT TACTC GAG
2351 2400
Sh1 (2337)
Sus1 (2317)
Sus3 (2258)
Consensus (2351) AGGCTGATGACCCTGACCGGCGTGTACGGGTTCTGGAAGTACGTGTCCAA
2401 2450
Sh1 (2387)
Sus1 (2367)
Sus3 (2308)
Consensus (2401) CCTGGAGAGGCGCGAGACCCGGCGCTACCT GAGATGTTCTACGC CTGA
2451 2500
Sh1 (2437)
Sus1 (2417)
Sus3 (2358)
Consensus (2451) AGTACCGCA CCTGGCGAGCACCGTGCCGCTGGCC T GA G AG
2501 2550
Sh1 (2481)
Sus1 (2461)
Sus3 (2408)
Consensus (2501) TAGC GC AGAA G GA TGCGTAACA GGCACAGGCCTGA G
2551 2600
Sh1 (2525)
Sus1 (2507)
Sus3 (2458)
Consensus (2551) AACGATC C G A TT G CTCGG GT GTCA CAATTCGC

Figure 9e

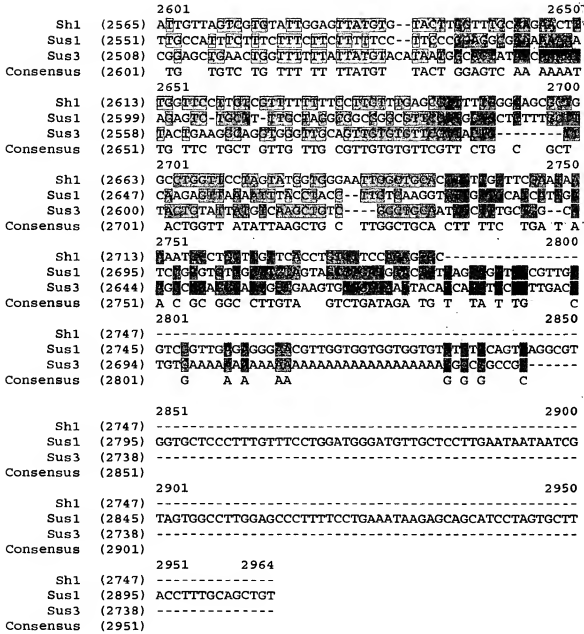
2601 2650
Sh1 (2565)
Sus1 (2551)
Sus3 (2508)
Consensus (2601)
2651 2700
Sh1 (2613)
Sus1 (2599)
Sus3 (2558)
Consensus (2651)
2701 2750
Sh1 (2663)
Sus1 (2647)
Sus3 (2600)
Consensus (2701)
2751 2800
Sh1 (2713)
Sus1 (2695)
Sus3 (2644)
Consensus (2751)
2801 2850
Sh1 (2747)
Sus1 (2745)
Sus3 (2694)
Consensus (2801)
2851 2900
Sh1 (2747)
Sus1 (2795)
Sus3 (2738)
Consensus (2851)
2901 2950
Sh1 (2747)
Sus1 (2845)
Sus3 (2738)
Consensus (2901)
2951 2964
Sh1 (2747)
Sus1 (2895) ACCTTTGCAGCTGT
Sus3 (2738)
Consensus (2951)

Figure 9f

CGCCAGTCGCCAGTCGCCACAGCCACACCACACCACACTAGCCGCGGCCGCGGGTAGGAG

CGCGCGCGGCGCGGCGGAACGACCCACCGGTGGCGGCAGCCATGTCTGCCCCGAAGCTGA

ACCGCAACGCGAGCATCCGGGACCGCGTCGAGGACACCCTCCACGCGCACCGCAACGAGC

TCGTCGCCCTCCTCTCCAAGTACGTGAACAAGGGGAAGGGCATCCTGCAGCCGCACCACA

TCCTCGACGCGCTCGACGAGGTCCAGGGCTCCGGGGTCCGCGCGCTCGCCGAGGGACCCT

TCCTCGACGTCCTCCGCTCCGCGCAGGAGGCGATCGTGCTGCCGCCG

Figure 10

Sorghum sequence from SEQ ID NO: 13 in SEQ ID NO: 11

ATGTCTGCCCCGAAGCTGAACCGCAACGCGAGCATCCGG

Maize sequence from SEQ ID NO: 1 in SEQ ID NO: 11

[redacted]g accgcgtcga ggacaccctc cacgcgcacc gcaacgagct 60
cgtcgccctc ctgtccaagt acgtgaacaa ggggaagggc atcctcgcagc cgcaccacat 120
cctcgacgcg ctcgacgagg tccagggctc cgggggccgc gcgctagccg agggaccctt 180
cctcgacgtc ctccgctccg cgcaggaggc gatcgtgctg ccgccgttcg tggccatcgc 240
ggtgcgcccg cgcccgggag tttgggagta cgtccgcgtc aacgttcacg agctcagcgt 300
cgagcagctc acagtctcgg agtacctccg cttcaaggag gagcttgtcg acggccagca 360
caatgatccc tacgttctcg agcttgactt cgagccgttc aatgtctcag tcccacgccc 420
aaatcggtca tcatctattg gaaacggtgt gcagttcctc aaccgacact tgtcctcaat 480
catgttccgc aacagggatt gcttggagcc cctgttggat ttcctccgtg gccaccggca 540
caaggggcat gttatgatgc ttaatgatag aatacaaagc ttggggaggc ttcagtctgt 600
gctgaccaaa gctgaggagc acttgtcaaa gctccctgct gacacaccat actcacaatt 660
tgcttataaa tttcaagagt ggggcctgga gaaaggttgg ggtgatacag caggacatgt 720
tttggaaatg atccatctcc ttctagacat cattcaggcg ccagacccat ctaccctaga 780
gaaattcctg gggaggatcc ccatgatttt taacgttgtt gtggtatccc ctcatggata 840
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ggaccaagtc cgtgcactag aaaatgagat ggttctccgt ttaaagaaac aagggcttga 960
tgtttcccca aagattctca ttgttactcg gctgatacca gatgcaaaag gaacatcatg 1020
caatcagcgg cttgagagaa ttagtggaac acagcatact tacatattac gagttccctt 1080
cagaaatgaa aatgggatac ttaagaaatg gatatcaaga tttgatgtgt ggccatatct 1140
ggaaacattt gctgaggatg ctgctggtga aattgctgct gaattacaag gtactccaga 1200
cttcataatt ggaaactaca gtgatggaaa tcttgtggcg tcattgctat cttacaagat 1260
gggaattacc cagtgcaaca ttgctcatgc tctggaaaag actaagtatc cagattcaga 1320
catattttgg aagaatttcg atgagaagta ccatttctcc tgccagttca ctgctgatat 1380
aattgctatg aacaatgctg atttta tcat caccagcaca taccaagaaa ttgctggaag 1440
caaaaatact gttggacagt atgagagtca tactgccttt actctgcctg gtctgtaccg 1500
agttgtccat gggatcgatg tcttcgatcc aaagttcaat atagtctctc ctggagctga 1560
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ccggtcaaag cccatcctct tctccatggc aagactcgac agggtgaaga acataacagg 1740
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tgccgggtac aatgatgtca acaagtccaa ggacagggaa gagatcgcgg agatagagaa 1860
gatgcatgaa ctcatcaaga cccacaactt gttcgggcag ttccgctgga tctctgccca 1920
gacaaacagg gcccgtaacg gcgagctcta tcgctacatc gctgataccc atggtgcttt 1980
cgtacagccg gccttgtatg aagcgttcgg tctcaccgtc gttgaggcca tgacctgtgg 2040
gcttcctact ttcgcgacgc tccatggagg tccagctgag atcatagagc atggcgtctc 2100
gggcttccac attgacccgt accaccccga acaggctgtt aatctgatgg ccgacttctt 2160
cgaccggtgc aagcaagacc cagatcactg ggtgaatata tctggagcag ggctgcagcg 2220
catatacgag aagtacacat ggaagatata ctcagagagg ttgatgacac tggccggggt 2280
ctacggtttc tggaagtacg tgtcgaagct cgagaggctg gagacgaggc gctaccttga 2340
gatgttctac atactgaagt tccgcgagct ggcgaagacc gtgccgcttg caattgacca 2400
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gaccttcagt aatttaggcg cggcagacgg tagccaataa aatgtgccgg agctgaactg 2520
gttttttatt atgtacataa tggcagtata acaaaattac tgaaggcagg tgggttgcag 2580
ttgtgtgttc gttactgttt actgtattat gtcaagctgt cggctgcaat ttctttgctg 2640
gcaagccgca ggcactggtg aagtgctgat aaatacatca tattctgttg acctgtgaaa 2700
aaaaaaaaaa aaaaaaaaaa aaaaaaaggg cggccgc

Figure 11